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Complete Genome Sequence of *Lactobacillus delbrueckii* subsp. *bulgaricus* Strain ND02▽

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***Lactobacillus delbrueckii* subsp. *bulgaricus* strain ND02 is a Chinese commercial dairy starter used for the manufacture of yoghurt. It was isolated from naturally fermented yak milk in Qinghai, China. Here, we report the main genome features of ND02 and several differences with two other published genomes of *Lactobacillus delbrueckii* subsp. *bulgaricus* strains.**

Lactobacillus delbrueckii subsp. *bulgaricus* and *Streptococcus thermophilus* are the most important strains used for industrial dairy starters. *L. delbrueckii* subsp. *bulgaricus* strain ND02 was isolated from naturally fermented yak milk in Qinghai, China (7). It has many excellent processing properties, such as moderate acidity, high viscosity, and water holding (7). This strain has been implemented in the industrial production of dairy starter cultures by Inner Mongolia Yili Industrial Group Company Limited, the largest dairy corporation in China.

Whole-genome sequencing of *L. delbrueckii* subsp. *bulgaricus* strain ND02 was performed with a combined strategy of 454 sequencing (6) and Solexa paired-end sequencing technology (1). Genomic libraries containing 8-kb inserts were constructed, and 62,098 paired-end reads and 127,000 single-end reads were generated using the GS FLX system, giving 28.0-fold coverage of the genome. A portion (95.3%) of these reads was assembled into two large scaffolds, including 283 nonredundant contigs, using the 454 Newbler assembler (454 Life Sciences, Branford, CT). A total of 8,778,388 reads (2.5-kb library) were generated to reach a depth of 218-fold coverage with an Illumina Solexa GA IIx (Illumina, San Diego, CA) and mapped to the scaffolds using Burrows-Wheeler Aligner (BWA) (4). The gaps between scaffolds were filled by sequencing PCR products using an ABI 3730 capillary sequencer. The genome analysis was performed as described previously (2, 3).

The complete genome sequence of ND02 contains a circular 2,125,753-bp chromosome and a 6,223-bp plasmid named LDBND_P, with mean GC contents of 49.56% and 44.66%, respectively. There are 2,177 genes in total, including 2,012 coding genes, 44 pseudogenes, 9 rRNA operons, and 94 tRNAs in the chromosome, as well as 6 coding genes in the plasmid.

Comparison of ATCC 11842 (9), ATCC BAA-365 (5), and ND02 genomes revealed that they were highly similar, with the exception of 416 encoding genes that are uniquely present in ND02 but not in the other two strains. Some of the unique genes formed six large insertion islands that were comprised by transposase, glutamate decarboxylase, acetyltransferase, glycosyltransferase, alcohol dehydrogenase, polysaccharide biosynthesis protein, and an exopolysaccharide (EPS) biosynthesis gene cluster.

Similar to the other two *L. delbrueckii* subsp. *bulgaricus* strains, ND02 partially inactivates several sugar transport and degradation pathways, with a preference for lactose in carbohydrate metabolism. Although some of the putative transporters for ribose (LDBND_0298) and ribokinase (LDBND_0152) are present in the genome, ND02 cannot grow on ribose as the only carbon source, presumably as a consequence of an incomplete pentose-phosphate pathway. Interestingly, a unique putative protein of raffinose permease (LDBND_1126) and raffinose operon transcriptional regulatory protein (RafR, LDBND_1126) are found in the genome of ND02 (without raffinose-specific PTS) by comparison of these three genomes. ND02 can grow on raffinose as the only carbon source, whereas the other two strains cannot grow (data not shown). This may be due to the raffinose permease of ND02, which was allosterically regulated for the uptake of non-PTS carbohydrates as a permease for lactose, maltose, and melibiose (8).

Nucleotide sequence accession numbers. The sequence and annotation of the *Lactobacillus delbrueckii* subsp. *bulgaricus* ND02 chromosome and plasmid are available from GenBank under accession numbers CP002341 and CP002342, respectively.

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